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Dekanat der Mathematisch-Naturwissenschaftlichen Fakultät

An alle
hauptamtlichen Professoren/innen
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Mathematisch-Naturwissenschaftlichen Fakultät

Promotionsverfahren von **Herrn M.Sc. Christian Schiffer**
**Auslage** der Dissertation und Gutachten sowie Termin der mündlichen Prüfung
<u>Anlage:</u> Einseitige Zusammenfassung der Dissertation

Sehr geehrte Damen und Herren,

in dem oben genannten Promotionsverfahren wird die Annahme der Dissertation

**Deep Neural Networks for Large-Scale Cytoarchitectonic Mapping of the Human Brain**

von den Berichterstattenden Prof. Dr. K. Amunts, Prof. Dr. S. Harmeling und Prof. Dr. W. Singer beantragt. Sie
kann zusammen mit den Gutachten in der Zeit
**vom 03.11.2022 bis 14.11.2022**

eingesehen werden. Bitte wenden Sie sich zur Einsicht an das Promotionsbüro (promotionmnf@hhu.de).

Einsprüche gegen diese Dissertation können nur zwei Tage nach der vorgenannten Frist
geltend gemacht werden. Erfolgt kein Einspruch, so gilt die Dissertation als angenommen
(§ 7 Ziffer (5) PO).

Sofern die Dissertation angenommen wird, findet die mündliche Prüfung am

**17.11.2022 um 11:00 Uhr**

im **22.01.HS 2B** statt. Als Prüferinnen bzw. Prüfer sind vorgesehen:
Prof. Dr. T. Dickscheid, Prof. Dr. M. Kollmann und Prof. Dr. S. Conrad.

Die Öffentlichkeit ist bei der Befragung nicht zugelassen.

Mit freundlichen Grüßen
im Auftrag

Nina Lönnendonker

# Abstract

**Title:** Deep Neural Networks for Large-Scale Cytoarchitectonic Mapping of the Human Brain

**Author:** Christian Schiffer

The analysis of microstructurally distinct cytoarchitectonic areas in the human brain provides the foundation to associate functional, physiological, genetic, molecular, and connectivity data with anatomically well-defined entities. Cytoarchitecture encompasses characteristic properties of neuronal cell distributions, including their shape, size, and spatial organization. High-resolution microscopic scans of cell-body stained histological brain sections enable the detailed analysis of these cytoarchitectonic properties, and thereby the brain's parcellation into structurally defined areas. The high inter-individual variability between brains necessitates the analysis of multiple brains to obtain a general picture of the human cytoarchitectonic organization. Modern high-throughput scanners enable the acquisition of microscopic image data on a large scale. However, established cytoarchitecture analysis methods are infeasible to handle the steadily increasing volume of data. This motivates the development of methods for the automated classification of cytoarchitectonic brain areas. Previous works on automated cytoarchitecture classification demonstrated the potential of deep learning methods to address this challenging task.

This work addresses automated cytoarchitectonic brain mapping at large scale. It introduces a deep learning method for interactive classification of individual brain areas across large series of histological brain sections. The method exploits the limited local variability of individual brain areas and requires minimal annotations. It integrates well with existing brain mapping workflows and provides the first practical method to support cytoarchitectonic mapping in large series of sections. Results of the presented workflow provide the foundations for creating 3D reconstructions of individual brain areas at previously unachieved spatial resolution.

The developed workflow focuses on the interactive application of deep learning for supporting cytoarchitectonic mapping. As a step towards fully automated brain mapping at large scale, this work further explores deep learning methods for classifying many different brain areas in multiple brain samples. It introduces a supervised contrastive learning method that learns to extract cytoarchitectonic features from large microscopic image datasets. Comprehensive evaluations demonstrate that learned features capture meaningful neuroanatomical properties and enable the accurate prediction of different cytoarchitectonic areas.

Finally, this work introduces a framework for cytoarchitectonic mapping using graph neural networks. It models the task as a node classification problem in a graph, enabling efficient integration of local cytoarchitectonic features with topological and contextual information. The approach takes inspiration from existing brain mapping workflows and achieves significantly improved classification performance.